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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/382,096

 DATE: 01/21/2000
 TIME: 13:54:21

Input Set: I382096.RAW

 This Raw Listing contains the General Information
 Section and up to first 5 pages.
ENTERED

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1  <110> APPLICANT: Outtrup, Helle
2      Nielsen, Bjarne Roenfeldt
3      Hedegaard, Lisbeth
4      Andersen, Jens Toenne
5  <120> TITLE OF INVENTION: Alkaline Bacillus Amylase
6  <130> FILE REFERENCE: 5442.400-US
7  <140> CURRENT APPLICATION NUMBER: US/09/382,096
8  <141> CURRENT FILING DATE: 1999-08-24
9  <150> EARLIER APPLICATION NUMBER: 0228/98
10 <151> EARLIER FILING DATE: 1998-02-18
11 <150> EARLIER APPLICATION NUMBER: 60/146,297
12 <151> EARLIER FILING DATE: 1998-02-27
13 <150> EARLIER APPLICATION NUMBER: 09/249,558
14 <151> EARLIER FILING DATE: 1999-02-12
15 <160> NUMBER OF SEQ ID NOS: 4
16 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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18 <211> LENGTH: 1646
19 <212> TYPE: DNA
20 <213> ORGANISM: Bacillus sp.
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22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)...(1646)
24 <221> NAME/KEY: sig_peptide
25 <222> LOCATION: (1)...(93)
26 <221> NAME/KEY: mat_peptide
27 <222> LOCATION: (94)...(1646)
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30      Met Gln Asn Thr Ala Lys Asn Ser Ile Trp Gln Arg Val Arg His Ser
31      -30                               -25                               -20
32      gcc att gcc tta tcc gct ctc agt tta tcc ttt ggc ctg cag gcc agc      96
33      Ala Ile Ala Leu Ser Ala Leu Ser Leu Ser Phe Gly Leu Gln Ala Ser
34      -15                               -10                               -5                               1
35      gag tta cca caa att cca cca cag cag gtg aac aac acc atg tac cag      144
36      Glu Leu Pro Gln Ile Pro Pro Gln Gln Val Asn Asn Thr Met Tyr Gln
37      5                               10                               15
38      gca ttt tat tgg gat gcc tac cct ggc ctt tgg gcc aat tta ccg gcc      192
39      Ala Phe Tyr Trp Asp Ala Tyr Pro Gly Leu Trp Ala Asn Leu Pro Ala
40      20                               25                               30
41      atg gcg gcc cct ttg gcc gag cgt ggc att acc tcg atg tgg ttg ccg      240
42      Met Ala Ala Pro Leu Ala Glu Arg Gly Ile Thr Ser Met Trp Leu Pro
43      35                               40                               45
44      ccc gcc gcc aaa ggc atg aat ggt act ttc agt gtc ggt tac gat gta      288

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45	Pro	Ala	Ala	Lys	Gly	Met	Asn	Gly	Thr	Phe	Ser	Val	Gly	Tyr	Asp	Val	
46	50					55					60					65	
47	tac	gat	ttc	tgg	gat	ctg	ggc	gag	ttt	aac	caa	aaa	ggc	acc	acc	gcc	336
48	Tyr	Asp	Phe	Trp	Asp	Leu	Gly	Glu	Phe	Asn	Gln	Lys	Gly	Thr	Thr	Ala	
49				70					75					80			
50	acc	cgt	tac	ggt	act	cgt	cag	cag	ctg	caa	caa	gca	ctg	agt	gct	ctg	384
51	Thr	Arg	Tyr	Gly	Thr	Arg	Gln	Gln	Leu	Gln	Gln	Ala	Leu	Ser	Ala	Leu	
52				85					90					95			
53	gac	caa	ctg	ggt	att	cag	gcc	tat	ttt	gat	gtg	gtg	ttt	aac	cac	cgc	432
54	Asp	Gln	Leu	Gly	Ile	Gln	Ala	Tyr	Phe	Asp	Val	Val	Phe	Asn	His	Arg	
55			100					105					110				
56	atg	ggc	gcc	gat	gca	cag	gag	aat	att	cct	ggc	ttt	ggc	ctg	gcc	tgg	480
57	Met	Gly	Ala	Asp	Ala	Gln	Glu	Asn	Ile	Pro	Gly	Phe	Gly	Leu	Ala	Trp	
58		115				120					125						
59	acc	gag	tat	cat	ctg	caa	ggt	cgt	cag	gcg	cat	tat	acc	cag	caa	aac	528
60	Thr	Glu	Tyr	His	Leu	Gln	Gly	Arg	Gln	Ala	His	Tyr	Thr	Gln	Gln	Asn	
61	130					135					140					145	
62	tgg	ggc	tac	ttg	tgg	cac	gac	ttt	gac	tgg	aac	tgg	acc	gcg	ttt	aat	576
63	Trp	Gly	Tyr	Leu	Trp	His	Asp	Phe	Asp	Trp	Asn	Trp	Thr	Ala	Phe	Asn	
64				150					155					160			
65	ggc	tcc	gac	aat	cag	ctc	tac	ccc	ggc	aaa	tgg	tgg	ggc	aat	acc	ttc	624
66	Gly	Ser	Asp	Asn	Gln	Leu	Tyr	Pro	Gly	Lys	Trp	Trp	Gly	Asn	Thr	Phe	
67			165					170					175				
68	cac	ttc	cct	tat	ttg	atg	ggt	gag	gat	gtc	gat	tac	aac	cgc	ttt	gaa	672
69	His	Phe	Pro	Tyr	Leu	Met	Gly	Glu	Asp	Val	Asp	Tyr	Asn	Arg	Phe	Glu	
70			180					185					190				
71	gtg	cag	cag	gaa	atg	aaa	gcc	tgg	ggc	gag	tgg	atc	atc	aac	agc	gtt	720
72	Val	Gln	Gln	Glu	Met	Lys	Ala	Trp	Gly	Glu	Trp	Ile	Ile	Asn	Ser	Val	
73		195					200					205					
74	ggc	ttt	agc	ggc	ttt	cgg	atg	gat	gcc	atc	gcc	cat	gtc	gat	acc	gat	768
75	Gly	Phe	Ser	Gly	Phe	Arg	Met	Asp	Ala	Ile	Ala	His	Val	Asp	Thr	Asp	
76	210					215				220				225			
77	ttt	acc	cgt	gac	tgg	atc	aat	cac	gtg	cag	tgg	gcc	acc	agt	gag	gat	816
78	Phe	Thr	Arg	Asp	Trp	Ile	Asn	His	Val	Gln	Trp	Ala	Thr	Ser	Glu	Asp	
79				230					235				240				
80	gtg	ttc	ttt	gtc	gct	gaa	gcc	tgg	gtc	agt	gat	atc	aac	ggc	tat	ctg	864
81	Val	Phe	Phe	Val	Ala	Glu	Ala	Trp	Val	Ser	Asp	Ile	Asn	Gly	Tyr	Leu	
82				245					250				255				
83	gat	gca	gtc	aat	acg	ccg	cat	ttg	cgc	gct	ttt	gat	ttc	aat	ttg	cgc	912
84	Asp	Ala	Val	Asn	Thr	Pro	His	Leu	Arg	Ala	Phe	Asp	Phe	Asn	Leu	Arg	
85			260					265					270				
86	gaa	gac	ttc	gtt	gct	tta	agc	agc	ggt	agc	aaa	gac	atg	cgt	tgg	tgg	960
87	Glu	Asp	Phe	Val	Ala	Leu	Ser	Ser	Gly	Ser	Lys	Asp	Met	Arg	Trp	Trp	
88		275					280					285					
89	ggc	ggt	ctg	gtc	aat	agc	cag	cac	cgt	gat	cgg	gcg	gtc	act	ttt	gtc	1008
90	Gly	Gly	Leu	Val	Asn	Ser	Gln	His	Arg	Asp	Arg	Ala	Val	Thr	Phe	Val	
91	290					295				300			305				
92	gat	aac	cac	gat	acc	agc	cgg	gcc	ggc	aac	cct	tat	ggc	atg	ccg	cag	1056
93	Asp	Asn	His	Asp	Thr	Ser	Arg	Ala	Gly	Asn	Pro	Tyr	Gly	Met	Pro	Gln	
94					310				315				320				

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96      Val Ile Asn Tyr Lys Asn Gln Ala Tyr Ala Tyr Ile Leu Leu Arg Glu
97              325                      330                      335
98      cat ggg gtg ccg act gtg ttt gcc cgc gat tac gac gaa ttt ggc atg      1152
99      His Gly Val Pro Thr Val Phe Ala Arg Asp Tyr Asp Glu Phe Gly Met
100             340                      345                      350
101     gcg cca acg ctg gat aaa ttg att gag gcg cgc cgc tac ttt gct tat      1200
102     Ala Pro Thr Leu Asp Lys Leu Ile Glu Ala Arg Arg Tyr Phe Ala Tyr
103             355                      360                      365
104     ggt cct ggc cat gag tac tcc ggc aat acc gag gcc gtc tac gcc tat      1248
105     Gly Pro Gly His Glu Tyr Ser Gly Asn Thr Glu Ala Val Tyr Ala Tyr
106     370                      375                      380                      385
107     gtg cgc gaa ggg ctt agc act gtg ccg ggt acc ggt ctg gtg atg ctg      1296
108     Val Arg Glu Gly Leu Ser Thr Val Pro Gly Thr Gly Leu Val Met Leu
109             390                      395                      400
110     ata tcg ggt cga aac tgg ggt ggt cag cag tcg ttc acc atc aac agc      1344
111     Ile Ser Gly Arg Asn Trp Gly Gly Gln Gln Ser Phe Thr Ile Asn Ser
112             405                      410                      415
113     cac cag ccg aat acc acc ttt tac gat tat acc ggc aat gtt agc ggc      1392
114     His Gln Pro Asn Thr Thr Phe Tyr Asp Tyr Thr Gly Asn Val Ser Gly
115             420                      425                      430
116     acg gtg acc acc aat gcg cag ggc tat ggc agc ttc ccg gtc act atg      1440
117     Thr Val Thr Thr Asn Ala Gln Gly Tyr Gly Ser Phe Pro Val Thr Met
118             435                      440                      445
119     acg gaa agt acc ggt tgg tca gtc tgg gta cca caa tcc aat ggt ggc      1488
120     Thr Glu Ser Thr Gly Trp Ser Val Trp Val Pro Gln Ser Asn Gly Gly
121     450                      455                      460                      465
122     act cag ccg gga tcc att acc ctg cgg atg acc aag gat gtt ggc tat      1536
123     Thr Gln Pro Gly Ser Ile Thr Leu Arg Met Thr Lys Asp Val Gly Tyr
124             470                      475                      480
125     ggc ttt tcg ttg ttc ttc acc ggc agc agt gcg gaa ctg acc aac tgg      1584
126     Gly Phe Ser Leu Phe Phe Thr Gly Ser Ser Ala Glu Leu Thr Asn Trp
127             485                      490                      495
128     ggc ggc ggt att gaa ggc acc tgg aca tcc ggt aat gtc tgg gaa gtg      1632
129     Gly Gly Gly Ile Glu Gly Thr Trp Thr Ser Gly Asn Val Trp Glu Val
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131     acc atc ccg gat cc      1646
132     Thr Ile Pro Asp
133             515
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138 <220> FEATURE:
139 <221> NAME/KEY: SIGNAL
140 <222> LOCATION: (1)...(31)
141 <400> SEQUENCE: 2
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144     Ala Ile Ala Leu Ser Ala Leu Ser Leu Ser Phe Gly Leu Gln Ala Ser

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145	-15	-10	-5	1
146	Glu Leu Pro Gln Ile Pro Pro Gln Gln Val Asn Asn Thr Met Tyr Gln			
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148	Ala Phe Tyr Trp Asp Ala Tyr Pro Gly Leu Trp Ala Asn Leu Pro Ala			
149	20	25	30	
150	Met Ala Ala Pro Leu Ala Glu Arg Gly Ile Thr Ser Met Trp Leu Pro			
151	35	40	45	
152	Pro Ala Ala Lys Gly Met Asn Gly Thr Phe Ser Val Gly Tyr Asp Val			
153	50	55	60	65
154	Tyr Asp Phe Trp Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Thr Ala			
155	70	75	80	
156	Thr Arg Tyr Gly Thr Arg Gln Gln Leu Gln Gln Ala Leu Ser Ala Leu			
157	85	90	95	
158	Asp Gln Leu Gly Ile Gln Ala Tyr Phe Asp Val Val Phe Asn His Arg			
159	100	105	110	
160	Met Gly Ala Asp Ala Gln Glu Asn Ile Pro Gly Phe Gly Leu Ala Trp			
161	115	120	125	
162	Thr Glu Tyr His Leu Gln Gly Arg Gln Ala His Tyr Thr Gln Gln Asn			
163	130	135	140	145
164	Trp Gly Tyr Leu Trp His Asp Phe Asp Trp Asn Trp Thr Ala Phe Asn			
165	150	155	160	
166	Gly Ser Asp Asn Gln Leu Tyr Pro Gly Lys Trp Trp Gly Asn Thr Phe			
167	165	170	175	
168	His Phe Pro Tyr Leu Met Gly Glu Asp Val Asp Tyr Asn Arg Phe Glu			
169	180	185	190	
170	Val Gln Gln Glu Met Lys Ala Trp Gly Glu Trp Ile Ile Asn Ser Val			
171	195	200	205	
172	Gly Phe Ser Gly Phe Arg Met Asp Ala Ile Ala His Val Asp Thr Asp			
173	210	215	220	225
174	Phe Thr Arg Asp Trp Ile Asn His Val Gln Trp Ala Thr Ser Glu Asp			
175	230	235	240	
176	Val Phe Phe Val Ala Glu Ala Trp Val Ser Asp Ile Asn Gly Tyr Leu			
177	245	250	255	
178	Asp Ala Val Asn Thr Pro His Leu Arg Ala Phe Asp Phe Asn Leu Arg			
179	260	265	270	
180	Glu Asp Phe Val Ala Leu Ser Ser Gly Ser Lys Asp Met Arg Trp Trp			
181	275	280	285	
182	Gly Gly Leu Val Asn Ser Gln His Arg Asp Arg Ala Val Thr Phe Val			
183	290	295	300	305
184	Asp Asn His Asp Thr Ser Arg Ala Gly Asn Pro Tyr Gly Met Pro Gln			
185	310	315	320	
186	Val Ile Asn Tyr Lys Asn Gln Ala Tyr Ala Tyr Ile Leu Leu Arg Glu			
187	325	330	335	
188	His Gly Val Pro Thr Val Phe Ala Arg Asp Tyr Asp Glu Phe Gly Met			
189	340	345	350	
190	Ala Pro Thr Leu Asp Lys Leu Ile Glu Ala Arg Arg Tyr Phe Ala Tyr			
191	355	360	365	
192	Gly Pro Gly His Glu Tyr Ser Gly Asn Thr Glu Ala Val Tyr Ala Tyr			
193	370	375	380	385
194	Val Arg Glu Gly Leu Ser Thr Val Pro Gly Thr Gly Leu Val Met Leu			

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195					390					395					400			
196	Ile	Ser	Gly	Arg	Asn	Trp	Gly	Gly	Gln	Gln	Ser	Phe	Thr	Ile	Asn	Ser		
197				405					410					415				
198	His	Gln	Pro	Asn	Thr	Thr	Phe	Tyr	Asp	Tyr	Thr	Gly	Asn	Val	Ser	Gly		
199			420					425				430						
200	Thr	Val	Thr	Thr	Asn	Ala	Gln	Gly	Tyr	Gly	Ser	Phe	Pro	Val	Thr	Met		
201		435					440				445							
202	Thr	Glu	Ser	Thr	Gly	Trp	Ser	Val	Trp	Val	Pro	Gln	Ser	Asn	Gly	Gly		
203	450				455				460						465			
204	Thr	Gln	Pro	Gly	Ser	Ile	Thr	Leu	Arg	Met	Thr	Lys	Asp	Val	Gly	Tyr		
205				470				475						480				
206	Gly	Phe	Ser	Leu	Phe	Phe	Thr	Gly	Ser	Ser	Ala	Glu	Leu	Thr	Asn	Trp		
207			485				490				495							
208	Gly	Gly	Gly	Ile	Glu	Gly	Thr	Trp	Thr	Ser	Gly	Asn	Val	Trp	Glu	Val		
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210	Thr	Ile	Pro	Asp														
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217	<221>	NAME/KEY:	CDS															
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225	Met	Gln	Asn	Thr	Ala	Lys	Asn	Ser	Ile	Trp	Gln	Arg	Val	Arg	His	Ser		
226		-30				-25					-20							
227	gcc	att	gcc	tta	tcc	gct	ctc	agt	tta	tcc	ttt	ggc	ctg	cag	gcc	agc		96
228	Ala	Ile	Ala	Leu	Ser	Ala	Leu	Ser	Leu	Ser	Phe	Gly	Leu	Gln	Ala	Ser		
229		-15			-10				-5						1			
230	gag	tta	cca	caa	att	cca	cca	cag	cag	gtg	aac	aac	acc	atg	tac	cag		144
231	Glu	Leu	Pro	Gln	Ile	Pro	Pro	Gln	Gln	Val	Asn	Asn	Thr	Met	Tyr	Gln		
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233	gca	ttt	tat	tgg	gat	gcc	tac	cct	ggc	ctt	tgg	gcc	aat	tta	ccg	gcc		

Input Set: I382096.RAW

Line ? Error/Warning

Original Text

333 W Line data has been corrected

Thr Asn Leu His Pro Ser Phe Asn Gly Gly P